```
==============================================================
```
Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=4; day=25; hr=15; min=56; sec=41; ms=329;]
```
==============================================================
```


```
**************************************************************
```
Reviewer Comments:

For SEQ ID # 40 through 45 and 48 through 53, numeric identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence."
```
**************************************************************
```

Application No: 10585149   Version No: 1.0

Input Set:

Output Set:

Started: 2008-04-09 18:38:03.989
Finished: 2008-04-09 18:38:06.159
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 170 ms
Total Warnings: 46
Total Errors: 0
No. of SeqIDs Defined: 53
Actual SeqID Count: 53

Error code   Error Description

W   402   Undefined organism found in <213> in SEQ ID (1)

W   402   Undefined organism found in <213> in SEQ ID (2)

W   402   Undefined organism found in <213> in SEQ ID (3)

W   213   Artificial or Unknown found in <213> in SEQ ID (6)

W   213   Artificial or Unknown found in <213> in SEQ ID (7)

W   213   Artificial or Unknown found in <213> in SEQ ID (8)

W   213   Artificial or Unknown found in <213> in SEQ ID (9)

W   213   Artificial or Unknown found in <213> in SEQ ID (10)

W   213   Artificial or Unknown found in <213> in SEQ ID (11)

W   213   Artificial or Unknown found in <213> in SEQ ID (12)

W   213   Artificial or Unknown found in <213> in SEQ ID (13)

W   213   Artificial or Unknown found in <213> in SEQ ID (14)

W   213   Artificial or Unknown found in <213> in SEQ ID (16)

W   213   Artificial or Unknown found in <213> in SEQ ID (17)

W   213   Artificial or Unknown found in <213> in SEQ ID (22)

W   213   Artificial or Unknown found in <213> in SEQ ID (23)

W   213   Artificial or Unknown found in <213> in SEQ ID (24)

W   213   Artificial or Unknown found in <213> in SEQ ID (25)

W   213   Artificial or Unknown found in <213> in SEQ ID (26)

W   213   Artificial or Unknown found in <213> in SEQ ID (27)

```
          Input Set:


          Output Set:



            Started:  2008-04-09 18:38:03.989
           Finished:  2008-04-09 18:38:06.159
            Elapsed:  0 hr(s) 0 min(s) 2 sec(s) 170 ms
     Total Warnings:  46
       Total Errors:  0
No. of SeqIDs Defined:  53
  Actual SeqID Count:  53
```

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30) This error has occured more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (40)
W 402	Undefined organism found in <213> in SEQ ID (41)
W 402	Undefined organism found in <213> in SEQ ID (42)
W 402	Undefined organism found in <213> in SEQ ID (43)
W 402	Undefined organism found in <213> in SEQ ID (44)
W 402	Undefined organism found in <213> in SEQ ID (45)
W 402	Undefined organism found in <213> in SEQ ID (48)
W 402	Undefined organism found in <213> in SEQ ID (49)
W 402	Undefined organism found in <213> in SEQ ID (50)
W 402	Undefined organism found in <213> in SEQ ID (51)
W 402	Undefined organism found in <213> in SEQ ID (52)
W 402	Undefined organism found in <213> in SEQ ID (53)

<110> KaloBios, Inc.
      Bebbington, Christopher Robert
      Yu, Bo

<120> Transactivation System for Mammalian
   Cells

<130> 73678-023

<140>   10585149
<141>   2008-04-09

<150> 04815827.3
<151>   2006-02-21

<150> US 60/533,917
<151> 2003-12-31

<160> 53

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 236
<212> PRT
<213> Hamster

<400> 1
Met Ala Gln Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
 1   5   10   15
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val
            20   25   30
Gly Asp Val Asp Ala Ala Pro Leu Gly Ala Ala Pro Thr Pro Gly Ile
        35   40   45
Phe Ser Phe Gln Pro Glu Ser Asn Pro Thr Pro Ala Val His Arg Asp
    50   55   60
Met Ala Ala Arg Thr Ser Pro Leu Arg Pro Ile Val Ala Thr Thr Gly
65   70   75   80
Pro Thr Leu Ser Pro Val Pro Pro Val Val His Leu Thr Leu Arg Arg
                85   90   95
Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe Ala Glu Met
                100   105   110
Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala
            115   120   125
Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile
        130   135   140
Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu Ser Val Asn
145   150   155   160
Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp Met Thr Glu
                165   170   175
Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn Gly Gly Trp
            180   185   190
Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Val Arg Pro Leu Phe Asp
        195   200   205

Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala Leu Val Gly
    210   215   220
Ala Cys Ile Thr Leu Gly Thr Tyr Leu Gly His Lys
225   230   235

<210> 2
<211> 195
<212> PRT
<213> hamster

<400> 2
Met Ala Gln Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
 1   5   10   15
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val
                20   25   30
Gly Asp Val Asp Ala Ala Ala Ala Ala Ser Pro Val Pro Pro Val
         35   40   45
Val His Leu Thr Leu Arg Arg Ala Gly Asp Asp Phe Ser Arg Arg Tyr
     50   55   60
Arg Arg Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe
65   70   75   80
Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp
                85   90   95
Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val
                100   105   110
Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn
         115   120   125
Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp
     130   135   140
Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro
145   150   155   160
Ser Val Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu
                165   170   175
Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Thr Tyr Leu
                180   185   190
Gly His Lys
        195

<210> 3
<211> 588
<212> DNA
<213> hamster

<400> 3
atggctcaag ctgggagaac agggtatgat aaccgagaga tcgtgatgaa gtacatccat   60
tataagctgt cacagagggg ctacgagtgg gatgtggag atgtggacgc cgcggccgcg   120
gccgcgagcc ccgtgccacc tgtggtccac ctgaccctcc gccgggctgg ggatgacttc   180
tcccgtcgct accgtcgcga cttcgcggag atgtccagtc agctgcacct gacgcccttc   240
accgcgaggg gacgctttgc tacggtggtg gaggaactct caggatgg ggtgaactgg   300
gggaggattg tggccttctt tgagttcggt ggggtcatgt gtgtggagag cgtcaacagg   360
gagatgtcac ccctggtgga caacatcgcc ctgtggatga ccgagtacct gaaccggcat   420
ctgcacacct ggatccagga taacgaggc tgggacgcat ttgtggaact gtacggcccc   480
agtgtgaggc ctctgtttga tttctcttgg ctgtctctga agaccctgct cagcctggcc   540
ctggtcgggg cctgcatcac tctgggtacc tacctgggcc acaagtga   588

<210> 4
<211> 289

<212> PRT
<213> Human adenovirus type 5

<400> 4
Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala
1   5   10   15
Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu
            20   25   30
Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu His Asp
        35   40   45
Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln
    50   55   60
Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu
65   70   75   80
Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser
            85   90   95
Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met
            100   105   110
Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Gly His Glu Ala Gly
        115   120   125
Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu Glu Phe Val Leu
        130   135   140
Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser Cys His Tyr His
145   150   155   160
Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser Leu Cys Tyr Met
            165   170   175
Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser Glu Pro Glu Pro
            180   185   190
Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg Pro Lys
            195   200   205
Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser Arg Glu
    210   215   220
Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn Thr Pro
225   230   235   240
Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro Val Ala
            245   250   255
Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu Asp Leu
            260   265   270
Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg Pro Arg
        275   280   285
Pro

<210> 5
<211> 986
<212> DNA
<213> Human adenovirus type 5

<400> 5
atgagacata ttatctgcca cggaggtgtt attaccgaag aaatggccgc cagtcttttg   60
gaccagctga tcgaagaggt actggctgat aatcttccac ctcctagcca ttttgaacca   120
cctacccttc acgaactgca tgatttagac gtgacggccc ccgaagatcc caacgaggag   180
gcggtttcgc agattttttc cgactctgta atgttggcgg tgcaggaagg gattgactta   240
ctcactttttc cgccggcgcc cggttctccg gagccgcctc acctttcccg gcagcccgag   300
cagccggagc agagagcctt gggtccggtt tctatgccaa accttgtacc ggaggtgatc   360
gatcttaccg gccacgaggc tggctttcca cccagtgacg acgaggatga agagggtgag   420
gagtttgtgt tagattatgt ggagcacccc gggcacggtt gcaggtcttg tcattatcac   480

```
cggaggaata cgggggaccc agatattatg tgttcgcttt gctatatgag gacctgtggc      540
atgtttgtct acagtaagtg aaaattatgg gcagtgggtg atagagtggt gggtttggtg      600
tggtaatttt tttttaatt tttacagttt tgtggtttaa agaattttgt attgtgattt       660
ttttaaaagg tcctgtgtct gaacctgagc ctgagcccga gccagaaccg gagcctgcaa      720
gacctacccg ccgtcctaaa atggcgcctg ctatcctgag acgcccgaca tcacctgtgt      780
ctagagaatg caatagtagt acggatagct gtgactccgg tccttctaac acacctcctg      840
agatacaccc ggtggtcccg ctgtgcccca ttaaaccagt tgccgtgaga gttggtgggc      900
gtcgccaggc tgtggaatgt atcgaggact tgcttaacga gcctgggcaa cctttggact      960
tgagctgtaa acgccccagg ccataa                                          986


<210> 6
<211> 39
<212> DNA
<213> Artificial Sequence


<220>
<223> primer


<400> 6
cccgaattcg ccgccaccat gagacatatt atctgccac                             39


<210> 7
<211> 28
<212> DNA
<213> Artificial Sequence


<220>
<223> primer


<400> 7
cccgtcgacc ttatggcctg gggcgttt                                         28


<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence


<220>
<223> primer


<400> 8
cccggtaccg ccgccaccat gagacatatt atctgccac                             39


<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence


<220>
<223> primer


<400> 9
cccgcggccg ccttatggcc tggggcgttt                                       30


<210> 10
<211> 25
<212> DNA
```

<213> Artificial Sequence

<220>
<223> primer

<400> 10
ggaggtgatc gatcttaccg gccac   25

<210> 11
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 11
cctacccttc acgaactgca tgatttagac gtgacg   36

<210> 12
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 12
cgtcacgtct aaatcatgca gttcgtgaag ggtagg   36

<210> 13
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 13
cccgaattcg ccgccaccat ggaggcttgg gagtgttt   38

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 14
cccgtcgacc aacattcatt cccgagggt   29

<210> 15
<211> 558
<212> DNA
<213> Human adenovirus type 5

<400> 15
gaattcgccg ccaccatgga ggcttgggag tgtttggaag attttctgc tgtgcgtaac   60
ttgctggaac agagctctaa cagtacctct tggttttgga ggtttctgtg gggctcatcc   120
caggcaaagt tagtctgcag aattaaggag gattacaagt gggaatttga agagctttg   180
aaatcctgtg gtgagctgtt tgattctttg aatctgggtc accaggcgct ttttccaagag   240
aaggtcatca agactttgga ttttttccaca ccggggcgcg ctgcggctgc tgttgctttt   300
ttgagtttta taaaggataa atggagcgaa gaaacccatc tgagcggggg gtacctgctg   360
gattttctgg ccatgcatct gtggagagcg gttgtgagac acaagaatcg cctgctactg   420
ttgtcttccg tccgcccggc gataataccg acggaggagc agcagcagca gcaggaggaa   480
gccaggcggc ggcggcagga gcagagccca tggaacccga gagccggcct ggaccctcgg   540
gaatgaatgt tggtcgac   558

<210> 16
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 16
cccgtcgacg ccgccaccat gccgcccaaa acccccccg   38

<210> 17
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 17
cccgcggccg ccggtcctga gatcctcatt tc   32

<210> 18
<211> 2824
<212> DNA
<213> Homo sapiens

<400> 18
gtcgacgccg ccaccatgcc gcccaaaacc ccccgaaaaa cggccgccac cgccgccgct   60
gccgccgcgg aaccccccggc accgccgccg ccgcccccctc ctgaggagga cccagagcag   120
gacagcggcc cggaggacct gcctctcgtc aggcttgagt ttgaagaaac agaagaacct   180
gatttttactg cattatgtca gaaattaaag ataccagatc atgtcagaga gagagcttgg   240
ttaacttggg agaaagtttc atctgtggat ggagtattgg gaggttatat tcaaaagaaa   300
aaggaactgt ggggaatctg tatctttatt gcacgagttg acctagatga gatgtcgttc   360
actttactga gctacagaaa aacatacgaa atcagtgtcc ataaattctt taacttacta   420
aaagaaattg ataccagtac caaagttgat aatgctatgt caagactgtt gaagaagtat   480
gatgtattgt ttgcactctt cagcaaattg gaaaggacat gtgaacttat atatttgaca   540
caacccagca gttcgatatc tactgaaata aattctgcat tggtgctaaa agtttcttgg   600
atcacatttt tattagctaa aggggaagta ttacaaatgg aagatgatct ggtgatttca   660
tttcagttaa tgctatgtgt ccttgactat tttattaaac tctcacctcc catgttgctc   720
aaagaaccat ataaaacagc tgttataccc attaatggtt cacctcgaac acccaggcga   780
ggtcagaaca ggagtgcacg gatagcaaaa caactagaaa atgatacaag aattattgaa   840
gttctctgta aagaacatga atgtaatata gatgaggtga aaaatgttta tttcaaaaat   900
tttatacctt ttatgaattc tcttggactt gtaacatcta atggacttcc agaggttgaa   960
aatctttcta aacgatacga agaaatttat cttaaaaata aagatctaga tcgaagatta   1020

```
tttttggatc atgataaaac tcttcagact gattctatag acagttttga aacacagaga      1080
acaccacgaa aaagtaacct tgatgaagag gtgaatataa ttcctccaca cactccagtt      1140
aggactgtta tgaacactat ccaacaatta atgatgattt taaattctgc aagtgatcaa      1200
ccttcagaaa atctgatttc ctattttaac aactgcacag tgaatccaaa agaaagtata      1260
ctgaaaagag tgaaggatat aggatacatc tttaaagaga aatttgctaa agctgtggga      1320
cagggttgtg tcgaaattgg atcacagcga tacaaacttg gagttcgctt gtattaccga      1380
gtaatggaat ccatgcttaa atcagaagaa gaacgattat ccattcaaaa ttttagcaaa      1440
cttctgaatg acaacatttt tcatatgtct ttattggcgt cgctcttga ggttgtaatg       1500
gccacatata gcagaagtac atctcagaat cttgattctg aacagattt gtctttccca       1560
tggattctga atgtgcttaa tttaaaagcc tttgattttt acaaagtgat cgaaagtttt      1620
atcaaagcag aaggcaactt gacaagagaa atgataaaac atttagaacg atgtgaacat      1680
cgaatcatgg aatcccttgc atggctctca gattcacctt tatttgatct tattaaacaa      1740
tcaaaggacc gagaaggacc aactgatcac cttgaatctg cttgtcctct taatcttcct      1800
ctccagaata atcacactgc agcagatatg tatctttctc ctgtaagatc tccaaagaaa      1860
aaaggttcaa ctacgcgtgt aaattctact gcaaatgcag agacacaagc aacctcagcc      1920
ttccagaccc agaagccatt gaaatctacc tctctttcac tgtttttataa aaaagtgtat      1980
cggctagcct atctccggct aaatacactt tgtgaacgcc ttctgtctga gcacccagaa      2040
ttagaacata tcatctggac ccttttccag cacaccctgc agaatgagta tgaactcatg      2100
agagacaggc atttggacca aattatgatg tgttccatgt atggcatatg caaagtgaag      2160
aatatagacc ttaaattcaa aatcattgta acagcataca aggatcttcc tcatgctgtt      2220
caggagacat tcaaacgtgt tttgatcaaa gaagaggagt atgattctat tatagtattc      2280
tataactcgg tcttcatgca gagactgaaa acaaatattt tgcagtatgc ttccaccagg      2340
cccccctacct tgtcaccaat acctcacatt cctcgaagcc cttacaagtt tcctagttca      2400
cccttacgga ttcctggagg gaacatctat atttcacccc tgaagagtcc atataaaatt      2460
tcagaaggtc tgccaacacc aacaaaaatg actccaagat caagaatctt agtatcaatt      2520
ggtgaatcat tcgggacttc tgagaagttc cagaaaataa atcagatggt atgtaacagc      2580
gaccgtgtgc tcaaaagaag tgctgaagga agcaaccctc ctaaaccact gaaaaaacta      2640
cgctttgata ttgaaggatc agatgaagca gatggaagta acatctccc aggagagtcc       2700
aaatttcagc agaaactggc agaaatgact tctactcgaa cacgaatgca aaagcagaaa      2760
atgaatgata gcatggatac ctcaaacaag gaagagaaat gaggatctca ggaccggcgg      2820
ccgc                                                                   2824
```

<210> 19
<211> 928
<212> PRT
<213> Homo sapiens

<400> 19
```
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala
1               5                   10                  15
Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Glu Glu Asp
            20                  25                  30
Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
        35                  40                  45
Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
    50                  55                  60
Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65                  70                  75                  80
Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
                85                  90                  95
Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Arg Val Asp Leu Asp Glu
            100                 105                 110
Met Ser Phe Thr Leu Leu Ser Tyr Arg Lys Thr Tyr Glu Ile Ser Val
        115                 120                 125
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
    130                 135                 140
Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
```

```
         145                      150                      155                      160
Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
                 165                      170                      175
Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
                 180                      185                      190
Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
         195                      200                      205
Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
         210                      215                      220
Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
225                      230                      235                      240
Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
                 245                      250                      255
Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
                 260                      265                      270
Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
         275                      280                      285
Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
         290                      295                      300
Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg
305                      310                      315                      320
Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Arg Arg Leu Phe
                 325                      330                      335
Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu
                 340                      345                      350
Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Ile
         355                      360                      365
Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln
         370                      375                      380
Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu
385                      390                      395                      400
Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu
                 405                      410
```